

## RAW SEQUENCE LISTING

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Application Serial Number: 10/534, 238

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## RAW SEQUENCE LISTING

DATE: 02/15/2006

PATENT APPLICATION: US/10/534,238

TIME: 10:12:16

Input Set : A:\u015763-7.txt

Output Set: N:\CRF4\02152006\J534238.raw

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3 <110> APPLICANT: FESENKO, Evgeny Evgenyevich
4     NOVOSELOV, Vladimir Ivanovich
5     YANIN, Vadim Alekseevich
6     LIPKIN, Valery Mikhaylovich
7     SHUVAEVA, Tatyana Maratovna
9 <120> TITLE OF INVENTION: ANTIOXIDANT PHARMACEUTICAL COMPOUND, METHOD FOR PRODUCING
10    POLYPEPTIDE AND METHOD OF CURE
12 <130> FILE REFERENCE: u015763-7
14 <140> CURRENT APPLICATION NUMBER: 10/534238
15 <141> CURRENT FILING DATE: 2005-05-06
17 <150> PRIOR APPLICATION NUMBER: PCT/RU03/00473
18 <151> PRIOR FILING DATE: 2003-11-05
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 715
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (44)..(715)
34 <400> SEQUENCE: 1
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36                                     Met Pro Gly Gly
37                                     1
39 ctg ctt ctc ggg gac gtg gct ccc aac ttt gag gcc aat acc acc gtc      103
40 Leu Leu Leu Gly Asp Val Ala Pro Asn Phe Glu Ala Asn Thr Thr Val
41 5      10      15      20
43 ggc cgc atc cgt ttc cac gac ttt ctg gga gac tca tgg ggc att ctc      151
44 Gly Arg Ile Arg Phe His Asp Phe Leu Gly Asp Ser Trp Gly Ile Leu
45      25      30      35
47 ttc tcc cac cct cgg gac ttt acc cca gtg tgc acc aca gag ctt ggc      199
48 Phe Ser His Pro Arg Asp Phe Thr Pro Val Cys Thr Thr Glu Leu Gly
49      40      45      50
51 aga gct gca aag ctg gca cca gaa ttt gcc aag agg aat gtt aag ttg      247
52 Arg Ala Ala Lys Leu Ala Pro Glu Phe Ala Lys Arg Asn Val Lys Leu
53      55      60      65
55 att gcc ctt tca ata gac agt gtt gag gac cat ctt gcc tgg agc aag      295
56 Ile Ala Leu Ser Ile Asp Ser Val Glu Asp His Leu Ala Trp Ser Lys
57      70      75      80
59 gat atc aat gct tac aat tgt gaa gag ccc aca gaa aag tta cct ttt      343
60 Asp Ile Asn Ala Tyr Asn Cys Glu Glu Pro Thr Glu Lys Leu Pro Phe
61 85      90      95      100

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63 ccc atc atc gat gat agg aat cgg gag ctt gcc atc ctg ttg ggc atg      391
64 Pro Ile Ile Asp Asp Arg Asn Arg Glu Leu Ala Ile Leu Leu Gly Met
65          105          110          115
67 ctg gat cca gca gag aag gat gaa aag ggc atg cct gtg aca gct cgt      439
68 Leu Asp Pro Ala Glu Lys Asp Glu Lys Gly Met Pro Val Thr Ala Arg
69          120          125          130
71 gtg gtg ttt gtt ttt ggt cct gat aag aag ctg aag ctg tct atc ctc      487
72 Val Val Phe Val Phe Gly Pro Asp Lys Lys Leu Lys Leu Ser Ile Leu
73          135          140          145
75 tac cca gct acc act ggc agg aac ttt gat gag att ctc agg gta gtc      535
76 Tyr Pro Ala Thr Thr Gly Arg Asn Phe Asp Glu Ile Leu Arg Val Val
77          150          155          160
79 atc tct ctc cag ctg aca gca gaa aaa agg gtt gcc acc cca gtt gat      583
80 Ile Ser Leu Gln Leu Thr Ala Glu Lys Arg Val Ala Thr Pro Val Asp
81 165          170          175          180
83 tgg aag gat ggg gat agt gtg atg gtc ctt cca acc atc cct gaa gaa      631
84 Trp Lys Asp Gly Asp Ser Val Met Val Leu Pro Thr Ile Pro Glu Glu
85          185          190          195
87 gaa gcc aaa aaa ctt ttc ccg aaa gga gtc ttc acc aaa gag ctc cca      679
88 Glu Ala Lys Lys Leu Phe Pro Lys Gly Val Phe Thr Lys Glu Leu Pro
89          200          205          210
91 tct ggc aag aaa tac ctc cgc tac aca ccc cag cct      715
92 Ser Gly Lys Lys Tyr Leu Arg Tyr Thr Pro Gln Pro
93          215          220
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97 <211> LENGTH: 224
98 <212> TYPE: PRT
99 <213> ORGANISM: Homo sapiens
101 <400> SEQUENCE: 2
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104 1          5          10          15
107 Asn Thr Thr Val Gly Arg Ile Arg Phe His Asp Phe Leu Gly Asp Ser
108          20          25          30
111 Trp Gly Ile Leu Phe Ser His Pro Arg Asp Phe Thr Pro Val Cys Thr
112          35          40          45
115 Thr Glu Leu Gly Arg Ala Ala Lys Leu Ala Pro Glu Phe Ala Lys Arg
116          50          55          60
119 Asn Val Lys Leu Ile Ala Leu Ser Ile Asp Ser Val Glu Asp His Leu
120 65          70          75          80
123 Ala Trp Ser Lys Asp Ile Asn Ala Tyr Asn Cys Glu Glu Pro Thr Glu
124          85          90          95
127 Lys Leu Pro Phe Pro Ile Ile Asp Asp Arg Asn Arg Glu Leu Ala Ile
128          100          105          110
131 Leu Leu Gly Met Leu Asp Pro Ala Glu Lys Asp Glu Lys Gly Met Pro
132          115          120          125
135 Val Thr Ala Arg Val Val Phe Val Phe Gly Pro Asp Lys Lys Leu Lys
136          130          135          140
139 Leu Ser Ile Leu Tyr Pro Ala Thr Thr Gly Arg Asn Phe Asp Glu Ile
140 145          150          155          160

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143 Leu Arg Val Val Ile Ser Leu Gln Leu Thr Ala Glu Lys Arg Val Ala
144                               165                               170                               175
147 Thr Pro Val Asp Trp Lys Asp Gly Asp Ser Val Met Val Leu Pro Thr
148                               180                               185                               190
151 Ile Pro Glu Glu Glu Ala Lys Lys Leu Phe Pro Lys Gly Val Phe Thr
152                               195                               200                               205
155 Lys Glu Leu Pro Ser Gly Lys Lys Tyr Leu Arg Tyr Thr Pro Gln Pro
156                               210                               215                               220
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160 <211> LENGTH: 574
161 <212> TYPE: DNA
162 <213> ORGANISM: Homo sapiens
165 <220> FEATURE:
166 <221> NAME/KEY: CDS
167 <222> LOCATION: (44)..(574)
169 <400> SEQUENCE: 3
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171                               Met Pro Gly Gly
172                               1
174 ctg ctt ctg ggg gac gtg gct ccc aac ttt gag gcc aat acc acc gtc      103
175 Leu Leu Leu Gly Asp Val Ala Pro Asn Phe Glu Ala Asn Thr Thr Val
176 5                               10                               15                               20
178 ggc cgc atc cgt ttc cac gac ttt ctg gga gac tca tgg ggc att ctg      151
179 Gly Arg Ile Arg Phe His Asp Phe Leu Gly Asp Ser Trp Gly Ile Leu
180                               25                               30                               35
182 ttc tcc cac cct cgg gac ttt acc cca gtg tgc acc aca gag ctt ggc      199
183 Phe Ser His Pro Arg Asp Phe Thr Pro Val Cys Thr Thr Glu Leu Gly
184                               40                               45                               50
186 aga gct gca aag ctg gca cca gaa ttt gcc aag agg aat gtt aag ttg      247
187 Arg Ala Ala Lys Leu Ala Pro Glu Phe Ala Lys Arg Asn Val Lys Leu
188                               55                               60                               65
190 att gcc ctt tca ata gac agt gtt gag gac cat ctt gcc tgg agc aag      295
191 Ile Ala Leu Ser Ile Asp Ser Val Glu Asp His Leu Ala Trp Ser Lys
192                               70                               75                               80
194 gat atc aat gct tac aat tgt gaa gag ccc aca gaa aag tta cct ttt      343
195 Asp Ile Asn Ala Tyr Asn Cys Glu Glu Pro Thr Glu Lys Leu Pro Phe
196 85                               90                               95                               100
198 ccc atc atc gat gat agg aat cgg gag ctt gcc atc ctg ttg ggc atg      391
199 Pro Ile Ile Asp Asp Arg Asn Arg Glu Leu Ala Ile Leu Leu Gly Met
200                               105                               110                               115
202 ctg gat cca gca gag aag gat gaa aag ggc atg cct gtg aca gct cgt      439
203 Leu Asp Pro Ala Glu Lys Asp Glu Lys Gly Met Pro Val Thr Ala Arg
204                               120                               125                               130
206 gtg gtg ttt gtt ttt ggt cct gat aag aag ctg aag ctg tct atc ctg      487
207 Val Val Phe Val Phe Gly Pro Asp Lys Lys Leu Lys Leu Ser Ile Leu
208                               135                               140                               145
210 tac cca gct acc act ggc agg aac ttt gat gag att ctg agg gta gtc      535
211 Tyr Pro Ala Thr Thr Gly Arg Asn Phe Asp Glu Ile Leu Arg Val Val
212                               150                               155                               160

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214 atc tct ctc cag ctg aca gca gaa aaa agg gtt gcc acc          574
215 Ile Ser Leu Gln Leu Thr Ala Glu Lys Arg Val Ala Thr
216 165                      170                      175
219 <210> SEQ ID NO: 4
220 <211> LENGTH: 177
221 <212> TYPE: PRT
222 <213> ORGANISM: Homo sapiens
224 <400> SEQUENCE: 4
226 Met Pro Gly Gly Leu Leu Leu Gly Asp Val Ala Pro Asn Phe Glu Ala
227 1                      5                      10                      15
230 Asn Thr Thr Val Gly Arg Ile Arg Phe His Asp Phe Leu Gly Asp Ser
231                      20                      25                      30
234 Trp Gly Ile Leu Phe Ser His Pro Arg Asp Phe Thr Pro Val Cys Thr
235                      35                      40                      45
238 Thr Glu Leu Gly Arg Ala Ala Lys Leu Ala Pro Glu Phe Ala Lys Arg
239                      50                      55                      60
242 Asn Val Lys Leu Ile Ala Leu Ser Ile Asp Ser Val Glu Asp His Leu
243 65                      70                      75                      80
246 Ala Trp Ser Lys Asp Ile Asn Ala Tyr Asn Cys Glu Glu Pro Thr Glu
247                      85                      90                      95
250 Lys Leu Pro Phe Pro Ile Ile Asp Asp Arg Asn Arg Glu Leu Ala Ile
251                      100                     105                     110
254 Leu Leu Gly Met Leu Asp Pro Ala Glu Lys Asp Glu Lys Gly Met Pro
255                      115                     120                     125
258 Val Thr Ala Arg Val Val Phe Val Phe Gly Pro Asp Lys Lys Leu Lys
259                      130                     135                     140
262 Leu Ser Ile Leu Tyr Pro Ala Thr Thr Gly Arg Asn Phe Asp Glu Ile
263 145                     150                     155                     160
266 Leu Arg Val Val Ile Ser Leu Gln Leu Thr Ala Glu Lys Arg Val Ala
267                      165                     170                     175
270 Thr
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277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Artificially generated
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288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
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299 <211> LENGTH: 27

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300 <212> TYPE: DNA  
301 <213> ORGANISM: artificial Sequence  
303 <220> FEATURE:  
304 <223> OTHER INFORMATION: Artificially generated  
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312 <212> TYPE: DNA  
313 <213> ORGANISM: Artificial Sequence  
315 <220> FEATURE:  
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318 <400> SEQUENCE: 8  
319 ccataccttcg aattcaactt aggtggc 27

VERIFICATION SUMMARY

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